

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 10/580,813  
Source: JFwP  
Date Processed by STIC: 6/19/06

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), **EFS Submission User Manual - ePAVE**)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

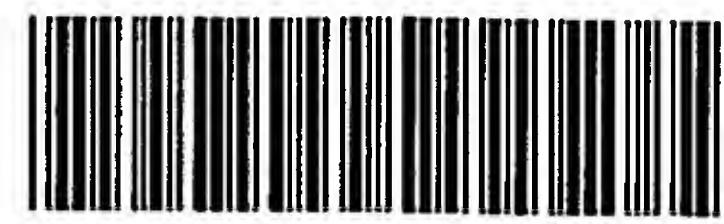
ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/580, 813

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- |    |   |   |
|----|---|---|
| 1  | ____ Wrapped Nucleic<br>Wrapped Aminos  | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor <b>after</b> creating it. Please adjust your right margin to .3; this will prevent "wrapping."   |
| 2  | ____ Invalid Line Length                | The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.  |
| 3  | ____ Misaligned Amino<br>Numbering      | The numbering under each 5 <sup>th</sup> amino acid is misaligned. <b>Do not use tab codes between numbers; use space characters,</b> instead.  |
| 4  | ____ Non-ASCII                          | The submitted file was <b>not</b> saved in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>   |
| 5  | ____ Variable Length                    | Sequence(s) ____ contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.   |
| 6  | ____ PatentIn 2.0<br>"bug"              | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>  |
| 7  | ____ Skipped Sequences<br>(OLD RULES)   | Sequence(s) ____ missing. If intentional, please insert the following lines for <b>each</b> skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped<br>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences. |
| 8  | ____ Skipped Sequences<br>(NEW RULES)   | Sequence(s) ____ missing. If <b>intentional</b> , please insert the following lines for <b>each</b> skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000  |
| 9  | ____ Use of n's or Xaa's<br>(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.   |
| 10 | ____ Invalid <213><br>Response          | Per 1.823 of Sequence Rules, the <b>only valid</b> <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence. (see item 11 below)  |
| 11 | ____ Use of <220>                       | Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is <b>MANDATORY</b> if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules  |
| 12 | ____ PatentIn 2.0<br>"bug"              | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.   |
| 13 | ____ Misuse of n/Xaa                    | "n" <b>can only</b> represent a single <u>nucleotide</u> ; "Xaa" <b>can only</b> represent a single <u>amino acid</u>   |



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/580,813

DATE: 06/19/2006  
TIME: 11:04:22

Input Set : A:\PTO.KD.txt  
Output Set: N:\CRF4\06192006\J580813.raw

3 <110> APPLICANT: Max Planck Gesellschaft zur Forderung der Wissenschaften  
5 <120> TITLE OF INVENTION: Substance binding human IgG Fc receptor IIb (Fc  
gamma  
6 RIIB)  
8 <130> FILE REFERENCE: 30287P\_WO HC  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/580,813  
C--> 11 <141> CURRENT FILING DATE: 2006-05-25  
13 <150> PRIOR APPLICATION NUMBER: EP03027000.3  
14 <151> PRIOR FILING DATE: 2003-11-26  
16 <160> NUMBER OF SEQ ID NOS: 11  
18 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

FcyI: <220> is shown

as an indication

Does Not Comply  
Corrected Diskette Needed

166 <210> SEQ ID NO: 5  
167 <211> LENGTH: 104  
168 <212> TYPE: PRT  
169 <213> ORGANISM: Unknown Organism

of error. It is

missing in submitted

insert a <220>

whenever <221>, <222>, or <223>

W--> 170 <220> FEATURE:

170 <223> OTHER INFORMATION: Description of Unknown Organism: sequence  
171 comprised by an antibody

EKG> 173 <400> SEQUENCE: 5

174 Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly  
175 1 5 10 15

177 Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr  
178 20 25 30

180 Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile  
181 35 40 45

183 Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly  
184 50 55 60

186 Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser  
187 65 70 75 80

189 Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr  
190 85 90 95

192 Thr Phe Gly Gly Thr Lys Leu  
193 100

241 <210> SEQ ID NO: 7

242 <211> LENGTH: 104

243 <212> TYPE: PRT

244 <213> ORGANISM: Unknown Organism) insert <220>

W--> 245 <220> FEATURE:

245 <223> OTHER INFORMATION: Description of Unknown Organism: sequence  
246 comprised by an antibody

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/580,813

DATE: 06/19/2006  
TIME: 11:04:22

Input Set : A:\PTO.KD.txt  
Output Set: N:\CRF4\06192006\J580813.raw

*EK* 248 <400> SEQUENCE: 7  
 249 Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser  
 250 1 5 10 15  
 252 Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr  
 253 20 25 30  
 255 Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly  
 256 35 40 45  
 258 Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys  
 259 50 55 60  
 261 Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met  
 262 65 70 75 80  
 264 Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr  
 265 85 90 95  
 267 Gly Pro Phe Ala Tyr Trp Gly Gln  
 268 100  
 316 <210> SEQ ID NO: 9  
 317 <211> LENGTH: 103  
 318 <212> TYPE: PRT  
 319 <213> ORGANISM: Unknown Organism *insert 12207*  
 W--> 320 <220> FEATURE: *insert 12207*  
 320 <223> OTHER INFORMATION: Description of Unknown Organism: sequence  
 comprised by an antibody  
*EK* 323 <400> SEQUENCE: 9  
 324 Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr  
 325 1 5 10 15  
 327 Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala  
 328 20 25 30  
 330 Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr  
 331 35 40 45  
 333 Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
 334 50 55 60  
 336 Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp  
 337 65 70 75 80  
 339 Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe  
 340 85 90 95  
 342 Gly Gly Gly Thr Lys Leu Glu  
 343 100  
 394 <210> SEQ ID NO: 11  
 395 <211> LENGTH: 112  
 396 <212> TYPE: PRT  
 397 <213> ORGANISM: Unknown Organism  
 W--> 398 <220> FEATURE: *insert 12207*  
 398 <223> OTHER INFORMATION: Description of Unknown Organism: sequence  
 comprised by an antibody  
*EK* 401 <400> SEQUENCE: 11  
 402 Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile  
 403 1 5 10 15  
 405 Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp  
 406 20 25 30

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/580,813

DATE: 06/19/2006  
TIME: 11:04:22

Input Set : A:\PTO.KD.txt  
Output Set: N:\CRF4\06192006\J580813.raw

408 Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp  
409 35 40 45  
411 Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser  
412 50 55 60  
414 Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser  
415 65 70 75 80  
417 Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg Asp  
418 85 90 95  
420 Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
421 100 105 110

**VERIFICATION SUMMARY**  
PATENT APPLICATION: US/10/580,813

DATE: 06/19/2006  
TIME: 11:04:23

Input Set : A:\PTO.KD.txt  
Output Set: N:\CRF4\06192006\J580813.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:170 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
L:173 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5  
L:245 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:248 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7  
L:320 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:323 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9  
L:398 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11  
L:401 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11

do not include foreign 10/580,813 S  
accent marks. They cannot be processed

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb (Fc gamma  
RIIb)

<130> 30287P\_WO HC

<1507> PCT/EP2004/013450

<1517> 2004-11-26

These are prior data

====